



## BLAST2 Search Results

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**Program: blastn**

**Sequence ID(s) :**

☐ 768320CB1 (LGcompseqsJAN2002) vs. gb129mam

RECEIVED

OCT 15 2002

NCBI-BLASTN 2.0.10 [Aug-26-1999]

TECH CENTER 1600/2000 

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Query= 768320CB1  
(1275 letters)

Database: gb129mam  
38,579 sequences; 40,433,150 total letters

```
Searching.....done
```

Sequences producing significant alignments:

Score (bits)	E Value
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<input checked="" type="checkbox"/>	<a href="#">g163228</a>	Bovine inorganic pyrophosphatase mRNA sequence.	1227	0.0
<input checked="" type="checkbox"/>	<a href="#">g9957596</a>	Sus scrofa RNA helicase (RHIV-1) mRNA, complete cds.	38	0.16
<input checked="" type="checkbox"/>	<a href="#">g6651078</a>	Ovis aries proviral endogenous Jaagsiekte sheep retr	38	0.16
<input checked="" type="checkbox"/>	<a href="#">g6851175</a>	Ovis aries Jaagsiekte sheep retrovirus-like element,	36	0.64
<input checked="" type="checkbox"/>	<a href="#">g6651074</a>	Ovis aries proviral endogenous Jaagsiekte sheep retr	36	0.64

>g163228 Bovine inorganic pyrophosphatase mRNA sequence.  
Length = 1266

Score = 1227 bits (619), Expect = 0.0  
Identities = 847/923 (91%).  
Strand = Plus / Plus

Query: 64 gcggcggcggcaggactccggcactatgagcggcttcagcacccaggagcgcgcgcgc 123  
 |||||  
 Sbjct: 44 gcggcggcggcgtgtcccgccacgatgagcagcttcagcagcaggagcgcgcgcgc 103

**Query:** 124 cttctccctggagtaccgagtccttctc caaaaatgagaaggacaatatata tctccatt 183  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
**Sbjct:** 104 cttcacccctcgagtaccgagtccttctc caaaaatga aaaaggacaatatata tctctccatt 163

Query: 184 tcatgatattccaatttatgcagataaggatgtgtttcacatggtagtgaagtaccag 243  
 . |||||  
 Sbjct: 164 tcatgatattccaatttatgcagataagggaagtgtttcacatggtcggtgaagtgccgcg 223

Query: 244 ctggtctaattgcaaaaatggagattgctacaaaggacccttttaaaccctatttaaacaaga 303

Score = 52.0 bits (26), Expect = 1e-05  
Identities = 32/34 (94%)  
Strand = Plus / Plus

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Score = 48.1 bits (24), Expect = 2e-04  
Identities = 51/60 (85%)  
Strand = Plus / Plus

Query: 1138 tcaactaagataacttttagcacatgcttaaataatcaaagcagttgtcatttgggaagtca 1197  
||||||| ||| ||||| | ||||| ||||| || ||||| ||||| |||||  
Sbjct: 1108 tcaactaaggtaacatttagttcctgcttaaataatcaaggcggttgtagtttgggaagtca 1167

>g9957596 Sus scrofa RNA helicase (RHIV-1) mRNA, complete cds.  
Length = 4024

Score = 38.2 bits (19), Expect = 0.16  
Identities = 22/23 (95%)  
Strand = Plus / Plus

Query: 864 ccagagccattgtggatgcttta 886  
||||||| ||||| ||||| ||||| |||||  
Sbjct: 1961 ccagagcccttgtggatgcttta 1983

>g6651078 Ovis aries proviral endogenous Jaagsiekte sheep  
retrovirus-like clone enJSRV 5.9A1 protease (pro) gene,  
complete cds; and unknown gene.  
Length = 6696

Score = 38.2 bits (19), Expect = 0.16  
Identities = 19/19 (100%)  
Strand = Plus / Plus

Query: 257 aaaatggagattgctacaa 275  
||||||| ||||| ||||| ||||| |||||  
Sbjct: 3378 aaaatggagattgctacaa 3396

>g6851175 Ovis aries Jaagsiekte sheep retrovirus-like element,  
complete sequence.  
Length = 7940

Score = 36.2 bits (18), Expect = 0.64  
Identities = 18/18 (100%)  
Strand = Plus / Plus

Query: 258 aaatggagattgctacaa 275  
||||||| ||||| ||||| ||||| |||||  
Sbjct: 3398 aaatggagattgctacaa 3415

>g6651074 Ovis aries proviral endogenous Jaagsiekte sheep  
retrovirus-like clone enJSRV 5f16 Gag (gag), protease  
(pro), and envelope protein (env) genes, complete cds.  
Length = 6916

Score = 36.2 bits (18), Expect = 0.64  
Identities = 18/18 (100%)  
Strand = Plus / Plus

Query: 258 aaatggagattgctacaa 275  
||||||| ||||| ||||| ||||| |||||  
Sbjct: 3398 aaatggagattgctacaa 3415

Database: gbl29mam  
Posted date: May 6, 2002 5:07 PM  
Number of letters in database: 40,433,150  
Number of sequences in database: 38,579